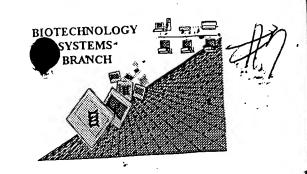


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable

Application Serial Number:	09/914549
Source:	PCTO9
Date Processed by STIC:	09/27/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS. PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1 821 - 1 825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2Kcompliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

	20/0.4/5/19 :
ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 09 914 549
ATTN: NEW RULES CASES	PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO
1Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6Patentin 2.0 "bug"	A "bug" in Patentin version 2.0 has caused the <220><223> section to be missing from amino acid sequences(s)
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to Include the skipped sequences.
8Skipped Sequences' (NEW RULES)	Sequence(s) missing. If Intentional, please insert the following lines for each skipped sequence <210> sequence id number <400> sequence id number 000
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown of the Artificial Sequence.
11Usc of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
Patentin 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
* *	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represen
13 Misuse of n	in can only be used to represent a single nucleotide in a nucleic acid sequences are any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

PCT09

RAW SEQUENCE LISTING DATE: 09/27/2001 PATENT APPLICATION: US/09/914,549 TIME: 12:13:28

```
4 <110> APPLICANT: Poustka, et al.
      6 <120> TITLE OF INVENTION: Protein (TP) That is Involved in the Development of the
Nervous
                                                                    Does Not Comply
              System
      9 <130> FILE REFERENCE: K 3008
                                                                Corrected Disk the Needed
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/914,549
C--> 13 <141> CURRENT FILING DATE: 2001-08-24
     14 <150> PRIOR APPLICATION NUMBER: PCT/DE00/00583
W--> 15 DE 199 08 423.8 - Erroneous text
     16 <151> PRIOR FILING DATE: (2000-02-28
W--> 17 (1999-02-26)
     19 <160> NUMBER OF SEQ ID NOS: 39
                                    Involid field 213 response: "DNA"

should be in field 212.

FYI: there is no field 214.
     21 <170> SOFTWARE: PatentIn Ver. 2.0
                                                                            1. Edit field 213
                                                                               delête 214
ERRORED SEQUENCES
                                                                            2. delete erroneous text
     5290 <210> SEQ ID NO: 39
                                    Also each prior. Filing date must appear in an individual field 151
                                                                            3. field 150 is required
     5291 <211> LENGTH: 81369
                                                                                before each 151
      5292 <213> ORGANISM: DNA
E--> 5293 (214) Homo sapiens
                                                                             4. Header 151 must
     5295 (212) TYPE:
5295 (400) SEQUENCE: 39
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                                                                                precede each prison
W--> 5295 <212> TYPE:
                                                                                   60 opelization date.
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      5302 actotactgg gaaatggtga ggtgtttcgt gaagacaatg gcaacacaga tgaagacatg
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      5304 cagatggagg aaataaagat ccagttgagc ttgttggcca gttggataga ggttgaggtt
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RAW SEQUENT LISTING PATENT APPLICATION: US/09/914,549

DATE: 09/27/2001 TIME: 12:13:29

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LISTING RAW SEQUEN PATENT APPLICATION: US/09/914,549

7 09/27/2001 TIME: 12:13:29

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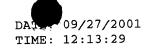
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RAW SEQUENT LISTING
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LISTING RAW SEQUEN PATENT APPLICATION: US/09/914,549

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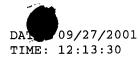
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DA1 09/27/2001 TIME: 12:13:30

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L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:15 M:259 W: Allowed number of lines exceeded, <150> PRIOR APPLICATION NUMBER:
L:17 M:259 W: Allowed number of lines exceeded, <151> PRIOR FILING DATE:
L:152 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:156 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:160 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:164 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:168 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:172 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:176 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:180 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:184 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:188 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:192 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:196 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:200 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:205 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:209 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:213 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:217 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:221 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:225 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:229 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:233 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
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 L:281 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:285 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:445 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:449 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:453 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:457 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:461 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
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 L:477 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:481 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
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VERIFICAT. SUMMARY
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Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF3\09272001\I914549.raw

L:485 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7 L:489 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7 L:493 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7 L:497 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7 L:501 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7 L:505 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7 L:5293 M:250 E: Invalid Amino Acid Number in Coding Region, SEQ ID:7 L:5293 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER L:5295 M:282 W: Numeric Field Identifier Missing, <212> is required.